



SEQUENCE LISTING

<110> SCHLESSINGER, JOSEPH
SAP, JAN M.
ULLRICH, AXEL
VOGEL, WOLFGANG
FUCHS, MIRIAM

<120> NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA

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<151> 1999-01-21

<150> 08/087,244
<151> 1993-07-01

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Leu Asn Gly Gly Gly Arg Ser Gly Met Phe Cys Ala Ile Gly Ile Val
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tac cct ctg cca aac act gta aaa gac ttc tgg aga tta gtg tat gat Tyr Pro Leu Pro Asn Thr Val Lys Asp Phe Trp Arg Leu Val Tyr Asp 1250 1255 1260	3792
tat ggc tgt acc tcc att gtg atg tta aac gaa gtc gac ttg tcc cag Tyr Gly Cys Thr Ser Ile Val Met Leu Asn Glu Val Asp Leu Ser Gln 1265 1270 1275 1280	3840
ggc tgc cct cag tac tgg cca gag gaa ggg atg cta cga tat ggc ccc Gly Cys Pro Gln Tyr Trp Pro Glu Glu Gly Met Leu Arg Tyr Gly Pro 1285 1290 1295	3888
atc caa gtg gaa tgt atg tct tgt tca atg gac tgt gat gtg atc aac Ile Gln Val Glu Cys Met Ser Cys Ser Met Asp Cys Asp Val Ile Asn 1300 1305 1310	3936

cgg att ttt agg ata tgc aat cta aca aga cca cag gaa ggt tat ctg 3984
 Arg Ile Phe Arg Ile Cys Asn Leu Thr Arg Pro Gln Glu Gly Tyr Leu
 1315 1320 1325
 atg gtg caa cag ttt cag tac cta gga tgg gct tct cat cga gaa gtg 4032
 Met Val Gln Gln Phe Gln Tyr Leu Gly Trp Ala Ser His Arg Glu Val
 1330 1335 1340
 cct gga tcc aaa agg tca ttc ttg aaa ctg ata ctt cag gtg gaa aag 4080
 Pro Gly Ser Lys Arg Ser Phe Leu Lys Leu Ile Leu Gln Val Glu Lys
 1345 1350 1355 1360
 tgg cag gag gaa tgg aag gaa ggg gaa ggc cgg acg att atc cac tgc 4128
 Trp Gln Glu Glu Trp Lys Glu Gly Glu Gly Arg Thr Ile Ile His Cys
 1365 1370 1375
 cta aat ggt ggc ggg cga agt ggc atg ttc tgt gct ata ggc atc gtt 4176
 Leu Asn Gly Gly Arg Ser Gly Met Phe Cys Ala Ile Gly Ile Val
 1380 1385 1390
 gtt gaa atg gtg aaa cgg caa aat gtt gtc gat gtt ttc cat gca gta 4224
 Val Glu Met Val Lys Arg Gln Asn Val Val Asp Val Phe His Ala Val
 1395 1400 1405
 aag aca ctg agg aac agc aag cca aac atg gtg gaa gcc cgg gag caa 4272
 Lys Thr Leu Arg Asn Ser Lys Pro Asn Met Val Glu Ala Pro Glu Gln
 1410 1415 1420
 tac cgt ttc tgc tat gat gta gct ttg gag tac ctg gaa tca tct 4317
 Tyr Arg Phe Cys Tyr Asp Val Ala Leu Glu Tyr Leu Glu Ser Ser
 1425 1430 1435
 tagttgggtg agactcttta aagtgcattcc atgaagaaac ctgtccatct attgagccag 4377
 cagctgttgt acctgttaca cttgtgcaga aagatttttaa tgtgggggggt gggagacttt 4437
 tacatttgag aggtaaaagt atttttttta tgaagttgtg tatcttaata aaaagaactg 4497
 aattagtttt tattactatt ataaagcatc aacatttcat gccacataaa attatattta 4557
 ataagaacca gattgaaatg agaacgtatt ggtgtttgta cagtgaacat gccacctttt 4617
 tccatggttt caggtagtgc agctaccaca tggt 4651

<210> 5
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 5
 Pro Pro Thr Asn Leu His Leu Glu Ala Asn Pro Asp Thr Gly Val Leu
 1 5 10 15
 Thr Val Ser Trp Glu Arg Ser Thr Thr Pro Asp Ile Thr Gly Tyr Arg
 20 25 30

Ile Thr Thr Thr Pro Thr Asn Gly Gln Gln Gly Asn Ser Leu Glu Glu
 35 40 45
 Val Val His Ala Asp Gln Ser Ser Cys Thr Phe Asp Asn Leu Ser Pro
 50 55 60
 Gly Leu Glu Tyr Asn Val Ser Val Tyr Thr Val Lys Asp Asp
 65 70 75

<210> 6
 <211> 155
 <212> PRT
 <213> Mus musculus

<400> 6
 Gly Gly Cys Leu Phe Asp Glu Pro Tyr Ser Thr Cys Gly Tyr Ser Gln
 1 5 10 15
 Ala Asp Glu Asp Phe Asn Trp Glu Gln Val Asn Thr Leu Thr Lys Pro
 20 25 30
 Thr Ser Asp Pro Trp Met Pro Ser Gly Ser Phe Met Leu Val Asn Thr
 35 40 45
 Ser Gly Lys Pro Glu Gly Gln Arg Ala His Leu Leu Leu Pro Gln Leu
 50 55 60
 Lys Glu Asn Asp Thr His Cys Ile Asp Phe His Tyr Phe Val Ser Ser
 65 70 75 80
 Lys Ser Asn Ala Ala Pro Gly Leu Leu Asn Val Tyr Val Lys Val Asn
 85 90 95
 Asn Gly Pro Leu Gly Asn Pro Ile Trp Asn Ile Ser Gly Asp Pro Thr
 100 105 110
 Arg Thr Trp His Arg Ala Glu Leu Ala Ile Ser Thr Phe Trp Pro Asn
 115 120 125
 Phe Tyr Gln Val Ile Phe Glu Val Val Thr Ser Gly His Gln Gly Tyr
 130 135 140
 Leu Ala Ile Asp Glu Val Lys Val Leu Gly His
 145 150 155

<210> 7
 <211> 154
 <212> PRT
 <213> Mus musculus

<400> 7
 Cys Lys Phe Gly Trp Gly Ser Gln Lys Thr Val Cys Asn Trp Gln His
 1 5 10 15
 Asp Ile Ser Ser Asp Leu Lys Trp Ala Val Leu Asn Ser Lys Thr Gly
 20 25 30

• • •

1 4 9

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<400> 8
Met Arg Thr Leu Gly Thr Cys Leu Ala Thr Leu Ala Gly Leu Leu Leu
  1          5          10          15

Thr Ala Ala Gly Glu Thr Phe Ser Gly Gly Cys Leu Phe Asp Glu Pro
      20          25          30

Tyr Ser Thr Cys Gly Tyr Ser Gln Ser Glu Gly Asp Asp Phe Asn Trp
      35          40          45

Glu Gln Val Asn Thr Leu Thr Lys Pro Thr Ser Asp Pro Trp Met Pro
      50          55          60

Ser Gly Ser Leu Met Leu Val Asn Ala Ser Gly Arg Pro Glu Gly Gln
  65          70          75          80

Arg Ala His Leu Leu Leu Pro Gln Leu Lys Glu Asn Asp Thr His Cys
      85          90          95

Ile Asp Phe His Tyr Phe Val Ser Ser Lys Ser Asn Ser Pro Pro Gly
      100          105          110

Leu Leu Asn Val Tyr Val Lys Val Asn Asn Gly Pro Leu Gly Asn Pro
      115          120          125

Ile Trp Asn Ile Ser Gly Asp Pro Thr Arg Thr Trp Asn Arg Ala Glu
      130          135          140

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Leu Ala Ile Ser Thr Phe Trp Pro Asn Phe Tyr Gln Val Ile Phe Glu
 145 150 155 160
 Val Ile Thr Ser Gly His Gln Gly Tyr Leu Ala Ile Asp Glu Val Lys
 165 170 175
 Val Leu Gly His Pro Cys Thr Arg Thr Pro His Phe Leu Arg Ile Gln
 180 185 190
 Asn Val Glu Val Asn Ala Gly Gln Phe Ala Thr Phe Gln Cys Ser Ala
 195 200 205
 Ile Gly Arg Thr Val Ala Gly Asp Arg Leu Trp Leu Gln Gly Ile Asp
 210 215 220
 Val Arg Asp Ala Pro Leu Lys Glu Ile Lys Val Thr Ser Ser Arg Arg
 225 230 235 240
 Phe Ile Ala Ser Phe Asn Val Val Asn Thr Thr Lys Arg Asp Ala Gly
 245 250 255
 Lys Tyr Arg Cys Met Ile Arg Thr Glu Gly Gly Val Gly Ile Ser Asn
 260 265 270
 Tyr Ala Glu Leu Val Val Lys Glu Pro Pro Val Pro Ile Ala Pro Pro
 275 280 285
 Gln Leu Ala Ser Val Gly Ala Thr Tyr Leu Trp Ile Gln Leu Asn Ala
 290 295 300
 Asn Ser Ile Asn Gly Asp Gly Pro Ile Val Ala Arg Glu Val Glu Tyr
 305 310 315 320
 Cys Thr Ala Ser Gly Ser Trp Asn Asp Arg Gln Pro Val Asp Ser Thr
 325 330 335
 Ser Tyr Lys Ile Gly His Leu Asp Pro Asp Thr Glu Tyr Glu Ile Ser
 340 345 350
 Val Leu Leu Thr Arg Pro Gly Glu Gly Gly Thr Gly Ser Pro Gly Pro
 355 360 365
 Ala Leu Arg Thr Arg Thr Lys Cys Ala Asp Pro Met Arg Gly Pro Arg
 370 375 380
 Lys Leu Glu Val Val Glu Val Lys Ser Arg Gln Ile Thr Ile Arg Trp
 385 390 395 400
 Glu Pro Phe Gly Tyr Asn Val Thr Arg Cys His Ser Tyr Asn Leu Thr
 405 410 415
 Val His Tyr Cys Tyr Gln Val Gly Gly Gln Glu Gln Val Arg Glu Glu
 420 425 430
 Val Ser Trp Asp Thr Glu Asn Ser His Pro Gln His Thr Ile Thr Asn
 435 440 445

Leu Ser Pro Tyr Thr Asn Val Ser Val Lys Leu Ile Leu Met Asn Pro
 450 455 460
 Glu Gly Arg Lys Glu Ser Gln Glu Leu Thr Val Gln Thr Asp Glu Asp
 465 470 475 480
 Leu Pro Gly Ala Val Pro Thr Glu Ser Ile Gln Gly Ser Thr Phe Glu
 485 490 495
 Glu Lys Ile Phe Leu Gln Trp Arg Glu Pro Thr Gln Thr Tyr Gly Val
 500 505 510
 Ile Thr Leu Tyr Glu Ile Thr Tyr Lys Ala Val Ser Ser Phe Asp Pro
 515 520 525
 Glu Ile Asp Leu Ser Asn Gln Ser Gly Arg Val Ser Lys Leu Gly Asn
 530 535 540
 Glu Thr His Phe Leu Phe Phe Gly Leu Tyr Pro Gly Thr Thr Tyr Ser
 545 550 555 560
 Phe Thr Ile Arg Ala Ser Thr Ala Lys Gly Phe Gly Pro Pro Ala Thr
 565 570 575
 Asn Gln Phe Thr Thr Lys Ile Ser Ala Pro Ser Met Pro Ala Tyr Glu
 580 585 590
 Leu Glu Thr Pro Leu Asn Gln Thr Asp Asn Thr Val Thr Val Met Leu
 595 600 605
 Lys Pro Ala Gln Ser Arg Gly Ala Pro Val Ser Val Tyr Gln Ile Val
 610 615 620
 Val Glu Glu Glu Arg Pro Arg Arg Thr Lys Lys Thr Thr Glu Ile Leu
 625 630 635 640
 Lys Cys Tyr Pro Val Pro Ile His Phe Gln Asn Ala Ser Leu Leu Asn
 645 650 655
 Ser Gln Tyr Tyr Phe Ala Ala Glu Phe Pro Ala Asp Ser Leu Gln Ala
 660 665 670
 Ala Gln Pro Phe Thr Ile Gly Asp Asn Lys Thr Tyr Asn Gly Tyr Trp
 675 680 685
 Asn Thr Pro Leu Leu Pro Tyr Lys Ser Tyr Arg Ile Tyr Phe Gln Ala
 690 695 700
 Ala Ser Arg Ala Asn Gly Glu Thr Lys Ile Asp Cys Val Gln Val Ala
 705 710 715 720
 Thr Lys Gly Ala Ala Thr Pro Lys Pro Val Pro Glu Pro Glu Lys Gln
 725 730 735
 Thr Asp His Thr Val Lys Ile Ala Gly Val Ile Ala Gly Ile Leu Leu
 740 745 750

Phe Val Ile Ile Phe Leu Gly Val Val Leu Val Met Lys Lys Arg Lys
 755 760 765
 Leu Ala Lys Lys Arg Lys Glu Thr Met Ser Ser Thr Arg Gln Glu Met
 770 775 780
 Thr Val Met Val Asn Ser Met Asp Lys Ser Tyr Ala Glu Gln Gly Thr
 785 790 795 800
 Asn Cys Asp Glu Ala Phe Ser Phe Met Asp Thr His Asn Leu Asn Gly
 805 810 815
 Arg Ser Val Ser Ser Pro Ser Ser Phe Thr Met Lys Thr Asn Thr Leu
 820 825 830
 Ser Thr Ser Val Pro Asn Ser Tyr Tyr Pro Asp Glu Thr His Thr Met
 835 840 845
 Ala Ser Asp Thr Ser Ser Leu Val Gln Ser His Thr Tyr Lys Lys Arg
 850 855 860
 Glu Pro Ala Asp Val Pro Tyr Gln Thr Gly Gln Leu His Pro Ala Ile
 865 870 875 880
 Arg Val Ala Asp Leu Leu Gln His Ile Thr Gln Met Lys Cys Ala Glu
 885 890 895
 Gly Tyr Gly Phe Lys Glu Glu Tyr Glu Ser Phe Phe Glu Gly Gln Ser
 900 905 910
 Ala Ser Trp Asp Val Ala Lys Lys Asp Gln Asn Arg Ala Lys Asn Arg
 915 920 925
 Tyr Gly Asn Ile Ile Ala Tyr Asp His Ser Arg Val Ile Leu Gln Pro
 930 935 940
 Val Glu Gly Asp Thr Asn Ser Asp Tyr Ile Asn Gly Asn Tyr Ile Asp
 945 950 955 960
 Gly Tyr His Arg Pro Asn His Tyr Ile Ala Thr Gln Gly Pro Met Gln
 965 970 975
 Glu Thr Ile Tyr Asp Phe Trp Arg Met Val Trp His Glu Asn Thr Ala
 980 985 990
 Ser Ile Ile Met Val Thr Asn Leu Val Glu Val Gly Arg Val Lys Cys
 995 1000 1005
 Cys Lys Tyr Trp Pro Asp Asp Thr Glu Ile Tyr Lys Asp Ile Lys Val
 1010 1015 1020
 Thr Leu Ile Glu Thr Glu Leu Leu Ala Glu Tyr Val Ile Arg Thr Phe
 1025 1030 1035 1040
 Ala Val Glu Lys Arg Gly Ile Ile Glu Ile Arg Glu Ile Arg Gln Phe
 1045 1050 1055

His Phe Thr Gly Trp Pro Asp His Gly Val Pro Tyr His Ala Thr Gly
 1060 1065 1070

Leu Leu Gly Phe Val Arg Gln Val Lys Ser Lys Ser Pro Pro Ser Ala
 1075 1080 1085

Gly Pro Leu Val Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Cys
 1090 1095 1100

Phe Ile Val Ile Asp Ile Met Leu Asp Met Ala Glu Arg Glu Gly Val
 1105 1110 1115 1120

Val Asp Ile Tyr Asn Cys Val Arg Glu Leu Arg Ser Arg Arg Val Asn
 1125 1130 1135

Met Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Ala Ile Leu
 1140 1145 1150

Glu Ala Cys Leu Cys Gly Asp Thr Ser Val Pro Ala Ser Gln Val Arg
 1155 1160 1165

Ser Leu Tyr Tyr Asp Met Asn Lys Leu Asp Pro Gln Thr Asn Ser Ser
 1170 1175 1180

Gln Ile Lys Glu Glu Phe Arg Thr Leu Asn Met Val Thr Pro Thr Leu
 1185 1190 1195 1200

Arg Val Glu Asp Cys Ser Ile Ala Leu Leu Pro Arg Asn His Glu Lys
 1205 1210 1215

Asn Arg Cys Met Asp Ile Leu Pro Pro Asp Arg Cys Leu Pro Phe Leu
 1220 1225 1230

Ile Thr Ile Asp Gly Glu Ser Ser Asn Tyr Ile Asn Ala Ala Leu Met
 1235 1240 1245

Asp Ser Tyr Lys Gln Pro Ser Ala Phe Ile Val Thr Gln His Pro Leu
 1250 1255 1260

Pro Asn Thr Val Lys Asp Phe Trp Arg Leu Val Leu Asp Tyr His Cys
 1265 1270 1275 1280

Thr Ser Val Val Met Leu Asn Asp Val Asp Pro Ala Gln Leu Cys Pro
 1285 1290 1295

Gln Tyr Trp Pro Glu Asn Gly Val His Arg His Gly Pro Ile Gln Val
 1300 1305 1310

Glu Phe Val Ser Ala Asp Leu Glu Glu Asp Ile Ile Ser Arg Ile Phe
 1315 1320 1325

Arg Ile Tyr Asn Ala Ala Arg Pro Gln Asp Gly Tyr Arg Met Val Gln
 1330 1335 1340

Gln Phe Gln Phe Leu Gly Trp Pro Met Tyr Arg Asp Thr Pro Val Ser
 1345 1350 1355 1360

Lys Arg Ser Phe Leu Lys Leu Ile Arg Gln Val Asp Lys Trp Gln Glu
 1365 1370 1375

Glu Tyr Asn Gly Gly Glu Gly Pro Thr Val Val His Cys Leu Asn Gly
 1380 1385 1390

Gly Gly Arg Ser Gly Thr Phe Cys Ala Ile Ser Ile Val Cys Glu Met
 1395 1400 1405

Leu Arg His Gln Arg Thr Val Asp Val Phe His Ala Val Lys Thr Leu
 1410 1415 1420

Arg Asn Asn Lys Pro Asn Met Val Asp Leu Leu Asp Gln Tyr Lys Phe
 1425 1430 1435 1440

Cys Tyr Glu Val Ala Leu Glu Tyr Leu Asn Ser Gly
 1445 1450

<210> 9

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gagccgcggc tcgaggttaac cgccatggat gtggcggccg

40

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

gctcacagct agttcagccc

20

<210> 11

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 11

ctacacccac atctaacgaa ccgtgaagca ggg

33

<210> 12

<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
cleavage motif

<400> 12
Arg Thr Lys Arg
1

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
modified cleavage motif

<400> 13
Leu Thr Asn Arg
1